

10/527370

DT09 Rec'd PCT/PTO 10 MAR 2005

1/8

SEQUENCE LISTING

<110> Toyo Boseki Kabushiki Kaisya

<120> Novel glycerol kinase, gene thereof and method for producing the glycerol kinase using the gene

<130> 030034PC1

<160> 6

<170> PatentIn version 2.1

<210> 1

<211> 505

<212> PRT

<213> Cellulomonas sp. JCM2471

<400> 1

Met Ala Asp Tyr Val Leu Ala Ile Asp Gln Gly Thr Thr Ser Ser Arg

1 5 10 15

Ala Ile Val Phe Asn His Ser Gly Glu Ile Tyr Ser Thr Gly Gln Leu

20 25 30

Glu His Asp Gln Ile Phe Pro Arg Ala Gly Trp Val Glu His Asn Pro

35 40 45

Glu Gln Ile Trp Asn Asn Val Arg Glu Val Val Gly Leu Ala Leu Thr

50 55 60

Arg Gly Asn Leu Thr His Glu Asp Ile Ala Ala Val Gly Ile Thr Asn

65 70 75 80

Gln Arg Glu Thr Ala Val Val Trp Asp Lys Thr Thr Gly Lys Pro Val

85 90 95

Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Gln Lys Ile Val Asp

100 105 110

Glu Leu Gly Gly Asp Glu Gly Ala Glu Lys Tyr Lys Ser Ile Val Gly

115	120	125	
Leu Pro Leu Ala Thr Tyr Phe Ser Gly Pro Lys Ile Lys Trp Ile Leu			
130	135	140	
Asp Asn Val Glu Gly Ala Arg Glu Lys Ala Glu Lys Gly Asp Leu Leu			
145	150	155	160
Phe Gly Asn Thr Asp Thr Trp Val Leu Trp Asn Met Thr Gly Gly Thr			
165	170	175	
Glu Gly Gly Val His Val Thr Asp Val Thr Asn Ala Ser Arg Thr Met			
180	185	190	
Leu Met Asp Leu Asp Thr Leu Ser Trp Arg Glu Asp Ile Ala Ala Asp			
195	200	205	
Met Gly Ile Pro Leu Ser Met Leu Pro Asp Ile Arg Ser Ser Ser Glu			
210	215	220	
Val Tyr Gly His Gly Arg Pro Arg Gly Leu Val Pro Gly Val Pro Ile			
225	230	235	240
Ala Gly Ile Leu Gly Asp Gln Gln Ala Ala Thr Phe Gly Gln Ala Cys			
245	250	255	
Phe Glu Val Gly Gln Ala Lys Asn Thr Tyr Gly Thr Gly Asn Phe Leu			
260	265	270	
Leu Leu Asn Thr Gly Thr Glu Lys Val Met Ser Lys Asn Gly Leu Leu			
275	280	285	
Thr Thr Val Cys Tyr Lys Ile Gly Asp Ala Pro Ala Val Tyr Ala Leu			
290	295	300	
Glu Gly Ser Ile Ala Val Thr Gly Ser Leu Val Gln Trp Leu Arg Asp			
305	310	315	320
Asn Leu Gly Met Phe Glu Asp Ala Pro Asp Val Glu Trp Leu Ala Gly			
325	330	335	
Lys Val Gln Asp Asn Gly Gly Ala Tyr Phe Val Pro Ala Phe Ser Gly			
340	345	350	

Leu Phe Ala Pro Tyr Trp Arg Pro Asp Ala Arg Gly Ala Leu Val Gly

355

360

365

Leu Thr Arg Tyr Val Asn Arg Asn His Ile Ala Arg Ala Ala Leu Glu

370

375

380

Ala Thr Ala Phe Gln Ser Arg Glu Val Val Asp Ala Met Asn Ala Asp

385

390

395

400

Ser Gly Val Asp Leu Thr Glu Leu Arg Val Asp Gly Gly Met Val Ala

405

410

415

Asn Glu Leu Leu Met Gln Phe Gln Ala Asp Gln Leu Gly Val Asp Val

420

425

430

Val Arg Pro Lys Val Ala Glu Thr Thr Ala Leu Gly Ala Ala Tyr Ala

435

440

445

Ala Gly Ile Ala Val Gly Phe Trp Lys Gly Glu Gln Asp Val Ile Asp

450

455

460

Asn Trp Ala Glu Asp Lys Arg Trp Ser Pro Ser Met Glu Ser Gly Glu

465

470

475

480

Arg Glu Arg Leu Tyr Arg Asn Trp Lys Lys Ala Val Thr Lys Thr Met

485

490

495

Glu Trp Val Asp Glu Asp Val Glu Gln

500

505

<210> 2

<211> 1515

<212> DNA

<213> Cellulomonas sp. JCM2471

<400> 2

atg gcc gac tac gtt ctc gcc atc gac cag ggg acc acg agc tcc cgg

48

Met Ala Asp Tyr Val Leu Ala Ile Asp Gln Gly Thr Thr Ser Ser Arg

1

5

10

15

gcc atc gtc ttc aac cac tcc ggg gag atc tac tcc acc ggg cag ctc	96
Ala Ile Val Phe Asn His Ser Gly Glu Ile Tyr Ser Thr Gly Gln Leu	
20 25 30	
gag cac gac cag atc ttc ccg cgc gcg ggc tgg gtc gag cac aac ccc	144
Glu His Asp Gln Ile Phe Pro Arg Ala Gly Trp Val Glu His Asn Pro	
35 40 45	
gag cag atc tgg aac aac gtg cgc gag gtc gtc ggt ctc gcc ctc acc	192
Glu Gln Ile Trp Asn Asn Val Arg Glu Val Val Gly Leu Ala Leu Thr	
50 55 60	
cga ggc aac ctc acg cac gag gac atc gcg gcc gtc ggc atc acg aac	240
Arg Gly Asn Leu Thr His Glu Asp Ile Ala Ala Val Gly Ile Thr Asn	
65 70 75 80	
cag cgc gag acg gcc gtc gtc tgg gac aag acc acg ggc aag ccc gtc	288
Gln Arg Glu Thr Ala Val Val Trp Asp Lys Thr Thr Gly Lys Pro Val	
85 90 95	
tac aac gcc atc gtc tgg cag gac acg cgc acc cag aag atc gtc gac	336
Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Gln Lys Ile Val Asp	
100 105 110	
gag ctc ggc ggc gac gag ggc gcc gag aag tac aag tcg atc gtc ggc	384
Glu Leu Gly Gly Asp Glu Gly Ala Glu Lys Tyr Lys Ser Ile Val Gly	
115 120 125	
ctg ccg ctc gcc acc tac ttc tcc ggc ccg aag atc aag tgg atc ctc	432
Leu Pro Leu Ala Thr Tyr Phe Ser Gly Pro Lys Ile Lys Trp Ile Leu	
130 135 140	
gac aac gtc gag ggt gcg cgc gag aag gcc gag aag ggc gac ctg ctg	480
Asp Asn Val Glu Gly Ala Arg Glu Lys Ala Glu Lys Gly Asp Leu Leu	
145 150 155 160	
ttc ggc aac acc gac acg tgg gtg ctg tgg aac atg acg ggc ggc acc	528
Phe Gly Asn Thr Asp Thr Trp Val Leu Trp Asn Met Thr Gly Gly Thr	

165	170	175	
gag ggc ggc gtg cac gtc acc gac gtg acc aac gcg tcg cgc acg atg			576
Glu Gly Gly Val His Val Thr Asp Val Thr Asn Ala Ser Arg Thr Met			
180	185	190	
ctc atg gac ctc gac acg ctc tcc tgg cgc gag gac atc gcc gcc gac			624
Leu Met Asp Leu Asp Thr Leu Ser Trp Arg Glu Asp Ile Ala Ala Asp			
195	200	205	
atg ggc atc ccg ctg tcg atg ctc ccc gac atc cgg tcg tcg tcc gag			672
Met Gly Ile Pro Leu Ser Met Leu Pro Asp Ile Arg Ser Ser Ser Glu			
210	215	220	
gtc tac ggc cac ggg cgc ccg cgc ggc ctc gtc ccc ggc gtc ccg atc			720
Val Tyr Gly His Gly Arg Pro Arg Gly Leu Val Pro Gly Val Pro Ile			
225	230	235	240
gcc ggc atc ctc ggc gac cag cag gca gcc acg ttc ggc cag gcg tgc			768
Ala Gly Ile Leu Gly Asp Gln Gln Ala Ala Thr Phe Gly Gln Ala Cys			
245	250	255	
ttc gag gtc ggc cag gcc aag aac acc tac ggc acc ggc aac ttc ctg			816
Phe Glu Val Gly Gln Ala Lys Asn Thr Tyr Gly Thr Gly Asn Phe Leu			
260	265	270	
ctg ctc aac acg ggc acg gag aag gtc atg agc aag aac ggc ctg ctc			864
Leu Leu Asn Thr Gly Thr Glu Lys Val Met Ser Lys Asn Gly Leu Leu			
275	280	285	
acg acg gtc tgc tac aag atc ggc gac gcg ccc gcg gtg tac gcg ctc			912
Thr Thr Val Cys Tyr Lys Ile Gly Asp Ala Pro Ala Val Tyr Ala Leu			
290	295	300	
gag ggc tcg atc gcc gtg acc ggc tcg ctc gtg cag tgg ctg cgc gac			960
Glu Gly Ser Ile Ala Val Thr Gly Ser Leu Val Gln Trp Leu Arg Asp			
305	310	315	320
aac ctg ggc atg ttc gag gac gcg ccc gac gtc gag tgg ctc gcg ggc			1008

Asn Leu Gly Met Phe Glu Asp Ala Pro Asp Val Glu Trp Leu Ala Gly	
325 330 335	
aag gtc cag gac aac ggc ggc gcc tac ttc gtg ccg gcg ttc tcc ggc	1056
Lys Val Gln Asp Asn Gly Gly Ala Tyr Phe Val Pro Ala Phe Ser Gly	
340 345 350	
ctg ttc gcg ccc tac tgg cgg ccc gac gcg cgc ggc gcg ctc gtc ggc	1104
Leu Phe Ala Pro Tyr Trp Arg Pro Asp Ala Arg Gly Ala Leu Val Gly	
355 360 365	
ctc acg cgg tac gtc aac cgc aac cac atc gcg cgc gcc gcg ctc gag	1152
Leu Thr Arg Tyr Val Asn Arg Asn His Ile Ala Arg Ala Ala Leu Glu	
370 375 380	
gcg acg gcg ttc cag agc cgc gag gtc gtc gac gcg atg aac gcc gac	1200
Ala Thr Ala Phe Gln Ser Arg Glu Val Val Asp Ala Met Asn Ala Asp	
385 390 395 400	
tcg ggc gtc gac ctc acc gag ctg cgc gtc gac ggc ggc atg gtc gcc	1248
Ser Gly Val Asp Leu Thr Glu Leu Arg Val Asp Gly Gly Met Val Ala	
405 410 415	
aac gag ctc ctc atg cag ttc cag gcc gac cag ctc ggc gtc gac gtc	1296
Asn Glu Leu Leu Met Gln Phe Gln Ala Asp Gln Leu Gly Val Asp Val	
420 425 430	
gtg cgg ccc aag gtc gcc gag acg acg gcg ctc ggt gcc gcg tac gcc	1344
Val Arg Pro Lys Val Ala Glu Thr Thr Ala Leu Gly Ala Ala Tyr Ala	
435 440 445	
gcg ggc atc gcc gtc ggc ttc tgg aag ggc gag cag gac gtc atc gac	1392
Ala Gly Ile Ala Val Gly Phe Trp Lys Gly Glu Gln Asp Val Ile Asp	
450 455 460	
aac tgg gcc gag gac aag cgc tgg agc ccg tcg atg gag tcc ggc gag	1440
Asn Trp Ala Glu Asp Lys Arg Trp Ser Pro Ser Met Glu Ser Gly Glu	
465 470 475 480	

cgc gag cgg ctg tac cgc aac tgg aag aag gcc gtg acg aag acg atg 1488
 Arg Glu Arg Leu Tyr Arg Asn Trp Lys Lys Ala Val Thr Lys Thr Met

485

490

495

gag tgg gtc gac gag gac gtg gag cag 1515
 Glu Trp Val Asp Glu Asp Val Glu Gln

500

505

<210> 3

<211> 23

<212> DNA

<213> synthetic DNA

<400> 3

tacgtsetsg csatcgacca ggg 23

<210> 4

<211> 27

<212> DNA

<213> synthetic DNA

<400> 4

ttcttgtgsa tgccstgscs sacgaag 27

<210> 5

<211> 23

<212> DNA

<213> synthetic DNA

<400> 5

atatcgttgc gctcgaccag ggc 23

<210> 6

<211> 23

<212> DNA

<213> synthetic DNA

<400> 6

tcgtgttctt cccacgcat cgc . 23